



SEQUENCE LISTING

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<110> COX, Vivienne, Frances
SMITH, Richard, Anthony, Godwin
ROWLING, Pamela, Jane, Elizabeth

<120> NON-IDENTICAL GENES AND THEIR APPLICATION IN IMPROVED MOLECULAR
ADJUVANTS

<130> 37945-0008

<140> US 09/582,761

<141> 2000-08-28

<150> PCT/GB98/03918

<151> 1998-12-30

<150> GB 9727512.7

<151> 1997-12-31

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<170> PatentIn version 3.0

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 Gly Met Thr Pro Thr Val Ile Ala Val His Tyr Leu Asp Gln Thr Glu
 20 25 30

 Gln Trp Glu Lys Phe Gly Ile Glu Lys Arg Gln Glu Ala Leu Glu Leu
 35 40 45

 Ile Lys Lys Gly Tyr Thr Gln Gln Leu Ala Phe Lys Gln Pro Ser Ser
 50 55 60

 Ala Tyr Ala Ala Phe Asn Asn Arg Pro Pro Ser Thr Trp Leu Thr Ala
 65 70 75 80

 Tyr Val Val Lys Val Phe Ser Leu Ala Ala Gln Leu Ile Ala Ile Asp
 85 90 95

 Ser His Val Leu Cys Gly Ala Val Lys Trp Leu Ile Leu Glu Lys Gln
 100 105 110

 Lys Pro Asp Gly Val Phe Gln Glu Asp Gly Pro Val Ile His Gln Glu
 115 120 125

 Met Ile Gly Gly Phe Arg Asn Ala Lys Glu Ala Asp Val Ser Leu Thr
 130 135 140

Ala Phe Val Leu Ile Ala Leu Gln Glu Ala Arg Asp Ile Cys Glu Gly
 145 150 155 160
 Gln Val Asn Ser Leu Pro Gly Ser Ile Asn Lys Ala Gly Glu Tyr Ile
 165 170 175
 Glu Ala Ser Tyr Met Asn Leu Gln Arg Pro Tyr Thr Val Ala Ile Ala
 180 185 190
 Gly Tyr Ala Leu Ala Leu Met Asn Lys Leu Glu Glu Pro Tyr Leu Gly
 195 200 205
 Lys Phe Leu Asn Thr Ala Lys Asp Arg Asn Arg Trp Glu Glu Pro Asp
 210 215 220
 Gln Gln Leu Tyr Asn Val Glu Ala Thr Ser Tyr Ala Leu Leu Ala Leu
 225 230 235 240
 Leu Leu Leu Lys Asp Phe Asp Ser Val Pro Pro Val Val Arg Trp Leu
 245 250 255
 Asn Glu Gln Arg Tyr Tyr Gly Gly Gly Tyr Gly Ser Thr Gln Ala Thr
 260 265 270
 Phe Met Val Phe Gln Ala Leu Ala Gln Tyr Gln Thr Asp Val Pro Asp
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 Glu Glu Phe Cys
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 20 25 30
 Gln Trp Glu Lys Phe Gly Ile Glu Lys Arg Gln Glu Ala Leu Glu Leu
 35 40 45
 Ile Lys Lys Gly Tyr Thr Gln Gln Leu Ala Phe Lys Gln Pro Ser Ser
 50 55 60
 Ala Tyr Ala Ala Phe Asn Asn Arg Pro Pro Ser Thr Trp Leu Thr Ala
 65 70 75 80
 Tyr Val Val Lys Val Phe Ser Leu Ala Ala Gln Leu Ile Ala Ile Asp
 85 90 95

Ser His Val Leu Cys Gly Ala Val Lys Trp Leu Ile Leu Glu Lys Gln
 100 105 110
 Lys Pro Asp Gly Val Phe Gln Glu Asp Gly Pro Val Ile His Gln Glu
 115 120 125
 Met Ile Gly Gly Phe Arg Asn Ala Lys Glu Ala Asp Val Ser Leu Thr
 130 135 140
 Ala Phe Val Leu Ile Ala Leu Gln Glu Ala Arg Asp Ile Cys Glu Gly
 145 150 155 160
 Gln Val Asn Ser Leu Pro Gly Ser Ile Asn Lys Ala Gly Glu Tyr Ile
 165 170 175
 Glu Ala Ser Tyr Met Asn Leu Gln Arg Pro Tyr Thr Val Ala Ile Ala
 180 185 190
 Gly Tyr Ala Leu Ala Leu Met Asn Lys Leu Glu Glu Pro Tyr Leu Gly
 195 200 205
 Lys Phe Leu Asn Thr Ala Lys Asp Arg Asn Arg Trp Glu Glu Pro Asp
 210 215 220
 Gln Gln Leu Tyr Asn Val Glu Ala Thr Ser Tyr Ala Leu Leu Ala Leu
 225 230 235 240
 Leu Leu Leu Lys Asp Phe Asp Ser Val Pro Pro Val Val Arg Trp Leu
 245 250 255
 Asn Glu Gln Arg Tyr Tyr Gly Gly Gly Tyr Gly Ser Thr Gln Ala Thr
 260 265 270
 Phe Met Val Phe Gln Ala Leu Ala Gln Tyr Gln Thr Asp Val Pro Asp
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 His Asp Leu Asn Met Asp Val Ser Phe His Leu Pro Ser Ser Gly Ser
 290 295 300
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Thr Pro Ala Gly
 305 310 315 320
 Ser Gly Glu Gln Asn Met Ile Gly Met Thr Pro Thr Val Ile Ala Val
 325 330 335
 His Tyr Leu Asp Gln Thr Glu Gln Trp Glu Lys Phe Gly Ile Glu Lys
 340 345 350
 Arg Gln Glu Ala Leu Glu Leu Ile Lys Lys Gly Tyr Thr Gln Gln Leu
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 Ala Phe Lys Gln Pro Ser Ser Ala Tyr Ala Ala Phe Asn Asn Arg Pro
 370 375 380
 Pro Ser Thr Trp Leu Thr Ala Tyr Val Val Lys Val Phe Ser Leu Ala
 385 390 395 400
 Ala Gln Leu Ile Ala Ile Asp Ser His Val Leu Cys Gly Ala Val Lys
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Trp Leu Ile Leu Glu Lys Gln Lys Pro Asp Gly Val Phe Gln Glu Asp
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 Glu Ala Asp Val Ser Leu Thr Ala Phe Val Leu Ile Ala Leu Gln Glu
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 Ala Arg Asp Ile Cys Glu Gly Gln Val Asn Ser Leu Pro Gly Ser Ile
 465 470 475 480
 Asn Lys Ala Gly Glu Tyr Ile Glu Ala Ser Tyr Met Asn Leu Gln Arg
 485 490 495
 Pro Tyr Thr Val Ala Ile Ala Gly Tyr Ala Leu Ala Leu Met Asn Lys
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 Leu Glu Glu Pro Tyr Leu Gly Lys Phe Leu Asn Thr Ala Lys Asp Arg
 515 520 525
 Asn Arg Trp Glu Glu Pro Asp Gln Gln Leu Tyr Asn Val Glu Ala Thr
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 Ser Tyr Ala Leu Leu Ala Leu Leu Leu Lys Asp Phe Asp Ser Val
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 Pro Pro Val Val Arg Trp Leu Asn Glu Gln Arg Tyr Tyr Gly Gly Gly
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 Tyr Gly Ser Thr Gln Ala Thr Phe Met Val Phe Gln Ala Leu Ala Gln
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 Tyr Gln Thr Asp Val Pro Asp His Asp Leu Asn Met Asp Val Ser Phe
 595 600 605
 His Leu Pro Ser Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 610 615 620
 Ser Gly Ser Thr Pro Ala Gly Ser Gly Glu Gln Asn Met Ile Gly Met
 625 630 635 640
 Thr Pro Thr Val Ile Ala Val His Tyr Leu Asp Gln Thr Glu Gln Trp
 645 650 655
 Glu Lys Phe Gly Ile Glu Lys Arg Gln Glu Ala Leu Glu Leu Ile Lys
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 Lys Gly Tyr Thr Gln Gln Leu Ala Phe Lys Gln Pro Ser Ser Ala Tyr
 675 680 685
 Ala Ala Phe Asn Asn Arg Pro Pro Ser Thr Trp Leu Thr Ala Tyr Val
 690 695 700
 Val Lys Val Phe Ser Leu Ala Ala Gln Leu Ile Ala Ile Asp Ser His
 705 710 715 720
 Val Leu Cys Gly Ala Val Lys Trp Leu Ile Leu Glu Lys Gln Lys Pro
 725 730 735

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Gly	Gly	Phe	Arg	Asn	Ala	Lys	Glu	Ala	Asp	Val	Ser	Leu	Thr	Ala	Phe
		755					760					765			
Val	Leu	Ile	Ala	Leu	Gln	Glu	Ala	Arg	Asp	Ile	Cys	Glu	Gly	Gln	Val
	770					775					780				
Asn	Ser	Leu	Pro	Gly	Ser	Ile	Asn	Lys	Ala	Gly	Glu	Tyr	Ile	Glu	Ala
785					790					795					800
Ser	Tyr	Met	Asn	Leu	Gln	Arg	Pro	Tyr	Thr	Val	Ala	Ile	Ala	Gly	Tyr
			805						810					815	
Ala	Leu	Ala	Leu	Met	Asn	Lys	Leu	Glu	Glu	Pro	Tyr	Leu	Gly	Lys	Phe
			820					825					830		
Leu	Asn	Thr	Ala	Lys	Asp	Arg	Asn	Arg	Trp	Glu	Glu	Pro	Asp	Gln	Gln
		835					840						845		
Leu	Tyr	Asn	Val	Glu	Ala	Thr	Ser	Tyr	Ala	Leu	Leu	Ala	Leu	Leu	Leu
	850					855					860				
Leu	Lys	Asp	Phe	Asp	Ser	Val	Pro	Pro	Val	Val	Arg	Trp	Leu	Asn	Glu
865					870					875					880
Gln	Arg	Tyr	Tyr	Gly	Gly	Gly	Tyr	Gly	Ser	Thr	Gln	Ala	Thr	Phe	Met
			885						890					895	
Val	Phe	Gln	Ala	Leu	Ala	Gln	Tyr	Gln	Thr	Asp	Val	Pro	Asp	His	Asp
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<223> DNA sequence of pBC66-01

<400> 32
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gtgtagataa ctacgatacg ggagggcctta ccatctggcc ccagtgtgtc aatgataaccg 180
cgagacccac gctcaccggc tccagattta tcagcaataa accagccagc cggaagggcc 240
gagcgcagaa gtgggtcctgc aactttatcc gcctccatcc agtctattaa ttggtgccgg 300
gaagctagag taagtagttc gccagttaat agtttgcgca acgttggtgc cattgctaca 360
ggcatcgttg tgtcacgctc gtcgtttggt atggcttcat tcagctccgg tccccaacga 420
tcaaggcgag ttacatgata ccccatgttg tgcaaaaaag cggttagctc cttegggtcct 480
ccgatcgttg tcagaagtaa gttggccgca gtgttatcac tcatgggttat ggcagcactg 540
cataattctc ttactgtcat gccatccgta agatgctttt ctgtgactgg tgagtactca 600
accaagtcac tctgagaata gtgtatgcgg cgaccgagtt gctcttgccc ggcgtcaaca 660
cgggataata ccgcgccaca tagcagaact taaaagtgc tcatcattgg aaaacgttct 720

tccggggcgaa aactctcaag gatcttaccg ctggtgagat ccagttcgat gtaaccact	780
cgtgcaccca actgatcttc agcatctttt actttcacca gcgtttctgg gtgagcaaaa	840
acaggaaggc aaaatgccgc aaaaaagga ataagggcg caccgaaatg ttgaatactc	900
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gaccagaccg aacagtggga gaagtccgc atagagaaga ggcaagaggc cctggagctc	2280
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 ccaaactcat caatgtatct tatcatgtct ggtcgactct agaactagta acgacgatca 3240
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<210> 33
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence of site directed mutagenesis oligonucleotide primer
 used to make pBP66-06

<400> 33
 ccagcagtgg atcctgctag agttctgagg 30

<210> 34
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence of site directed mutagenesis primer used to make
 pBP-06

<400> 34
 cctcagaact ctagcaggat ccactgctgg 30

<210> 35
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence of oligonucleotide #50391

<400> 35
ccagcagtggtg ctcttcctgc ttctgcagga tc

32

<210> 36
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence of oligonucleotide #50392

<400> 36
gatcctgcag aagcaggaag agccactgct gg

32

<210> 37
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of (C3d)3 expressed in baculovirus/Sf9

<400> 37
Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1 5 10 15
Trp Ala Pro Ala Pro Thr Arg Ala Gly Ser Arg Ser Thr Pro Ala Gly
20 25 30
Ser Gly Glu Gln Asn Met Ile Gly Met Thr Pro Thr Val Ile Ala Val
35 40 45
His Tyr Leu Asp Gln Thr Glu Gln Trp Glu Lys Phe Gly Ile Glu Lys
50 55 60
Arg Gln Glu Ala Leu Glu Leu Ile Lys Lys Gly Tyr Thr Gln Gln Leu
65 70 75 80
Ala Phe Lys Gln Pro Ser Ser Ala Tyr Ala Ala Phe Asn Asn Arg Pro
85 90 95
Pro Ser Thr Trp Leu Thr Ala Tyr Val Val Lys Val Phe Ser Leu Ala
100 105 110
Ala Gln Leu Ile Ala Ile Asp Ser His Val Leu Cys Gly Ala Val Lys
115 120 125
Trp Leu Ile Leu Glu Lys Gln Lys Pro Asp Gly Val Phe Gln Glu Asp
130 135 140
Gly Pro Val Ile His Gln Glu Met Ile Gly Gly Phe Arg Asn Ala Lys
145 150 155 160
Glu Ala Asp Val Ser Leu Thr Ala Phe Val Leu Ile Ala Leu Gln Glu
165 170 175
Ala Arg Asp Ile Cys Glu Gly Gln Val Asn Ser Leu Pro Gly Ser Ile
180 185 190

Asn	Lys	Ala	Gly	Glu	Tyr	Ile	Glu	Ala	Ser	Tyr	Met	Asn	Leu	Gln	Arg
	195						200					205			
Pro	Tyr	Thr	Val	Ala	Ile	Ala	Gly	Tyr	Ala	Leu	Ala	Leu	Met	Asn	Lys
	210					215					220				
Leu	Glu	Glu	Pro	Tyr	Leu	Gly	Lys	Phe	Leu	Asn	Thr	Ala	Lys	Asp	Arg
225					230					235				240	
Asn	Arg	Trp	Glu	Glu	Pro	Asp	Gln	Gln	Leu	Tyr	Asn	Val	Glu	Ala	Thr
			245						250				255		
Ser	Tyr	Ala	Leu	Leu	Ala	Leu	Leu	Leu	Lys	Asp	Phe	Asp	Ser	Val	
		260					265					270			
Pro	Pro	Val	Val	Arg	Trp	Leu	Asn	Glu	Gln	Arg	Tyr	Tyr	Gly	Gly	Gly
		275					280					285			
Tyr	Gly	Ser	Thr	Gln	Ala	Thr	Phe	Met	Val	Phe	Gln	Ala	Leu	Ala	Gln
	290					295					300				
Tyr	Gln	Thr	Asp	Val	Pro	Asp	His	Asp	Leu	Asn	Met	Asp	Val	Ser	Phe
305					310					315				320	
His	Leu	Pro	Ser	Ser	Gly	Ser	Glu	Glu	Phe						
				325					330						

<210> 38
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence of oligo for modification of bacterial vector
 pBroc413

<400> 38
 tatgagatct cccgggggat cctagcggcc gctgca

36

<210> 39
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA sequence of oligo for modification of bacterial vector
 pBroc413

<400> 39
 gcggccgcta ggatcccccg ggagatctca

30

<210> 40
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of peptide for trifunctional linker

 <400> 40
 Ala Lys Ala Lys Ala Lys
 1 5

 <210> 41
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> DNA sequence of site directed mutagenesis oligonucleotide used to
 modify pBP66-06

 <400> 41
 ccacccgagc cggtaccaga tcta 24

 <210> 42
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> DNA sequence of site directed mutagenesis oligonucleotide used to
 modify pBP66-06

 <400> 42
 ggtagatctg gtaccggctc gggtagg 26

 <210> 43
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> DNA sequence of PCR primer used to amplify C3d monomer

 <400> 43
 cgagccatat gggtaccacc ccagc 25

 <210> 44
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> DNA sequence of PCR primer used to amplify C3d monomer

 <400> 44
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<210> 45
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> DNA sequence of mutagenic oligo giving addition of C-terminal cystein

<400> 45

ggatctgaag agttctgctg aggatcctat taaagc

36

<210> 46
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> DNA sequence of mutagenic oligo giving addition of C-terminal cystein

<400> 46

gctttaatag gatcctcagc agaactcttc agatcc

36